

FIG. 1

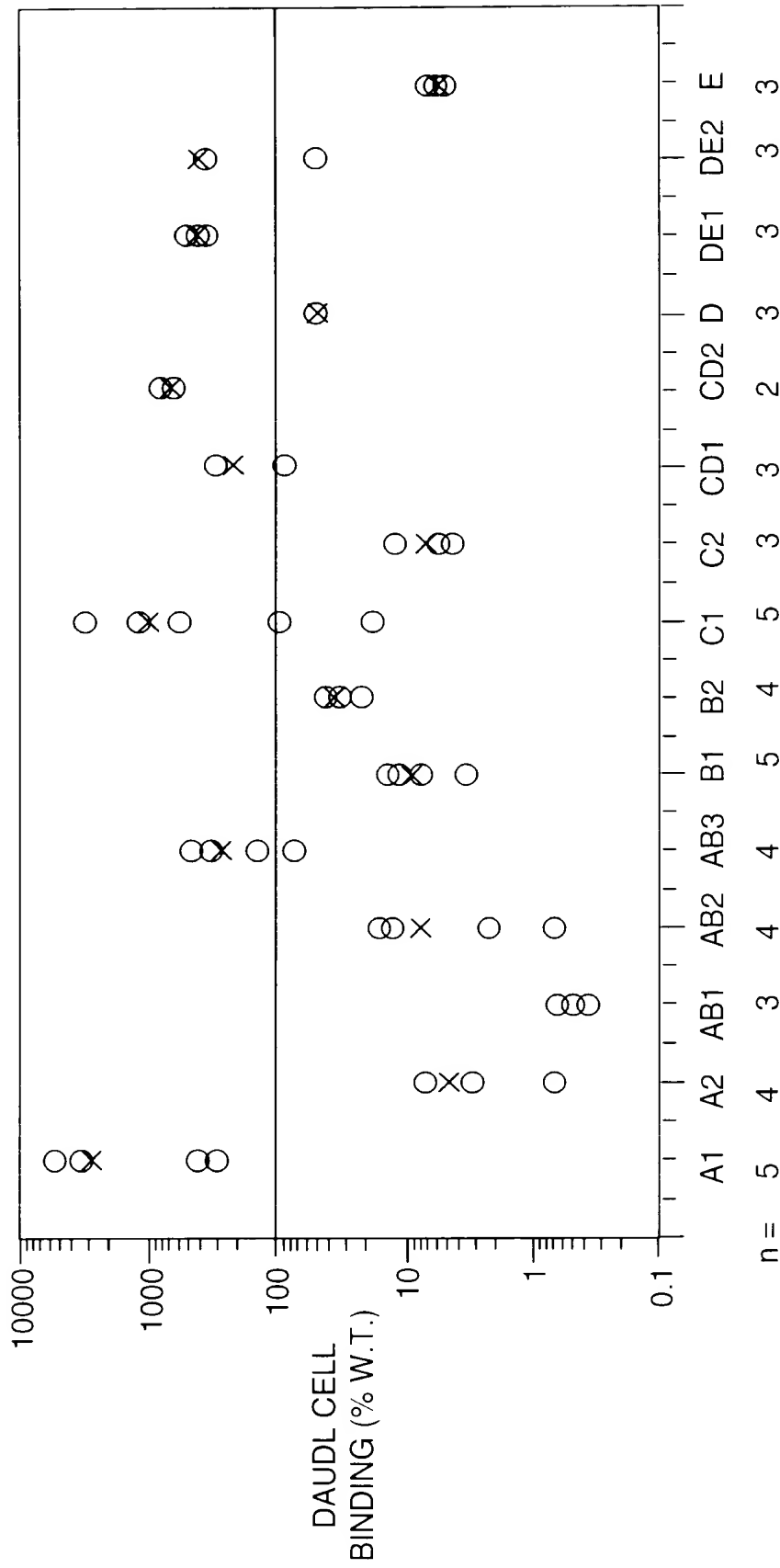


FIG. 2

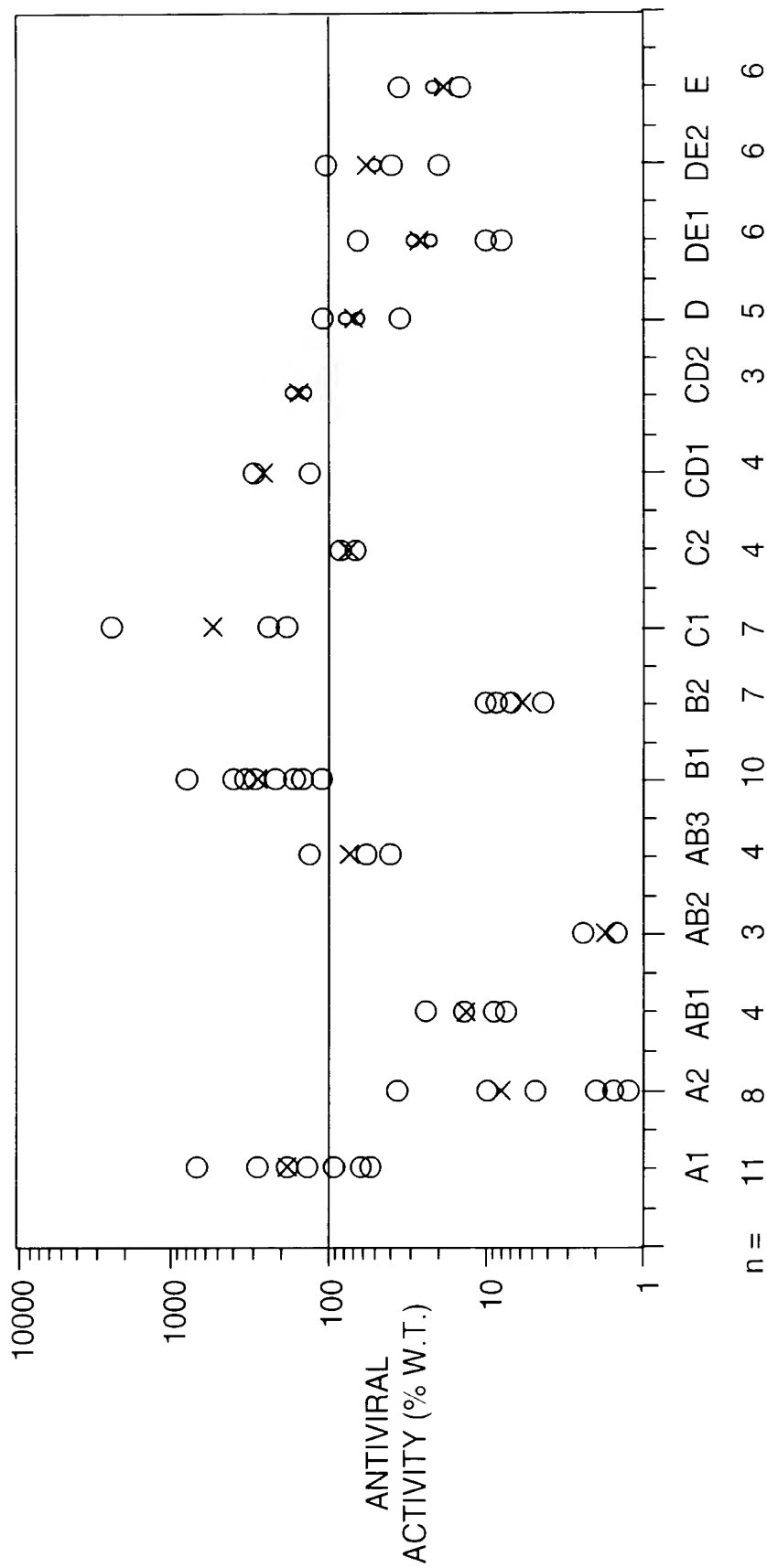


FIG. 3

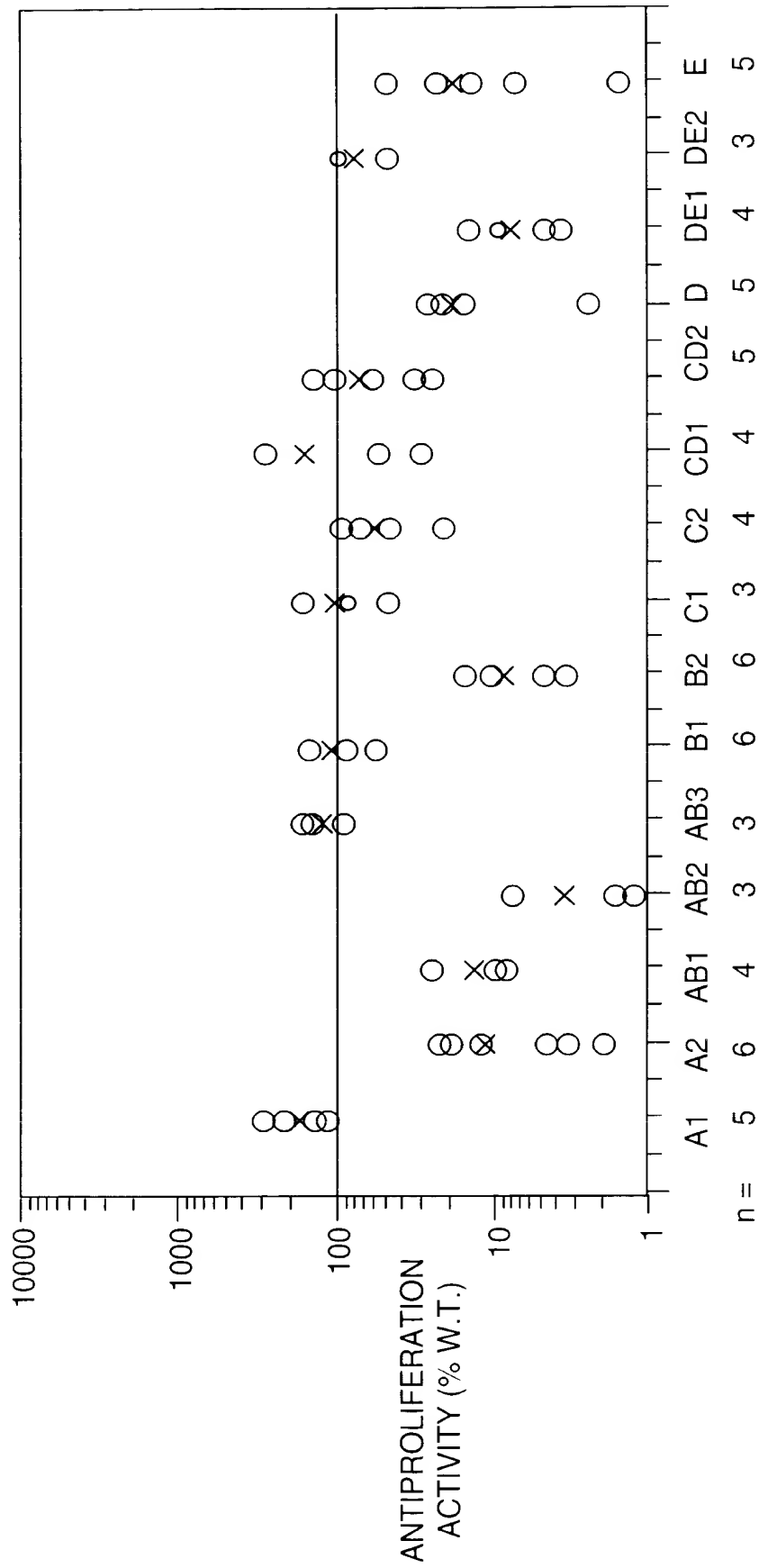


FIG. 4

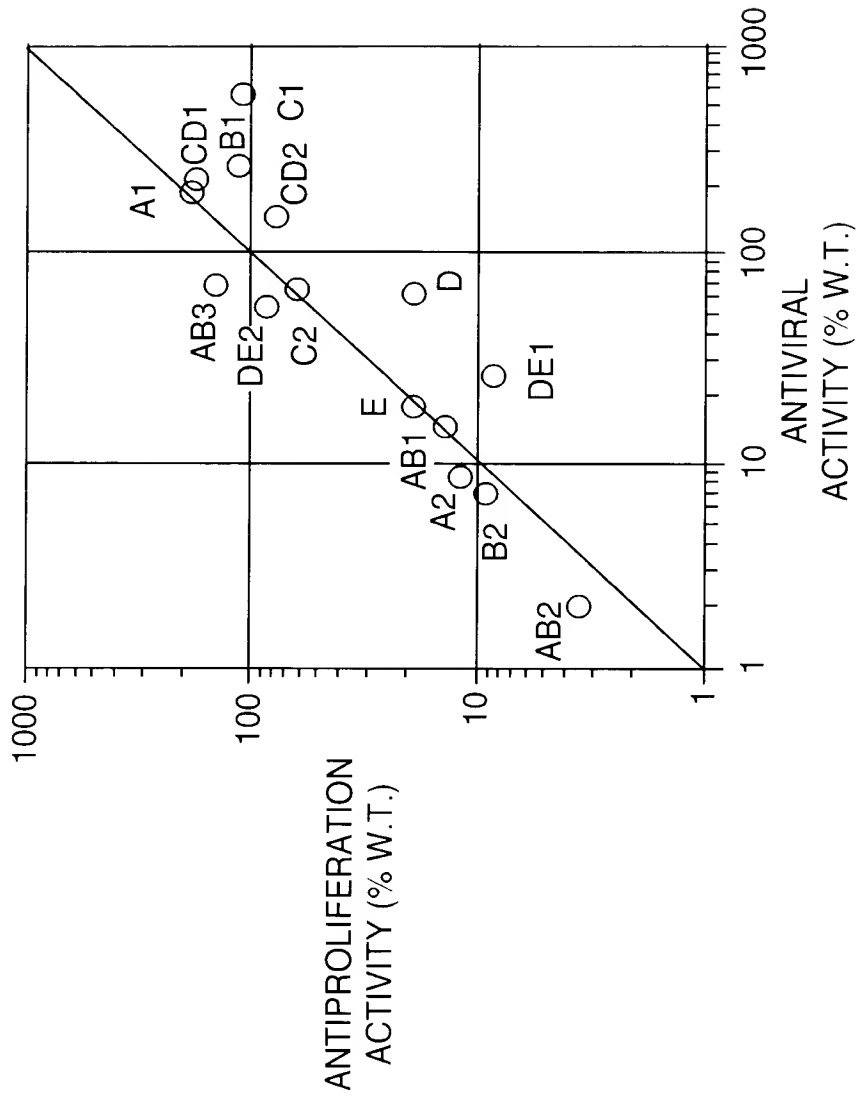


FIG. 5

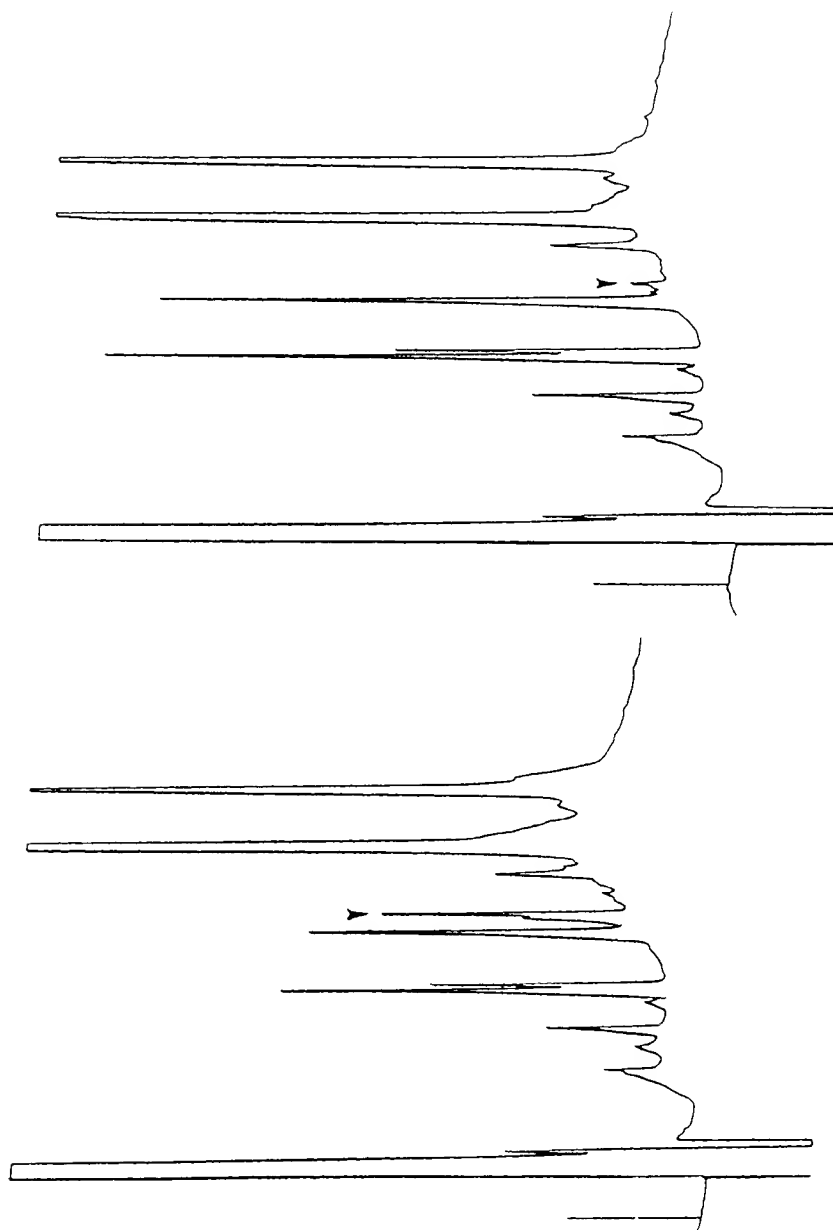


FIG. 6A

FIG. 6B

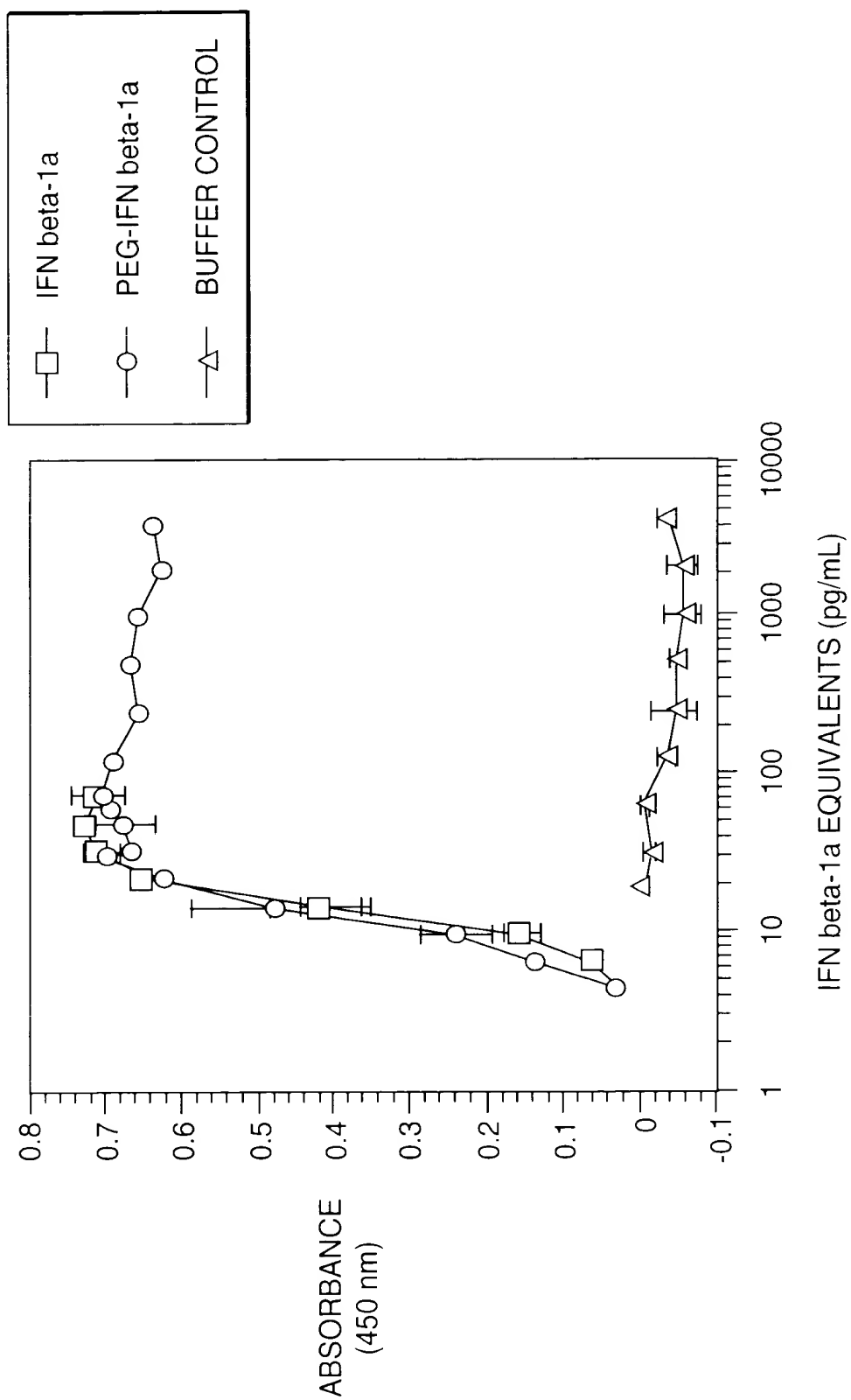


FIG. 7

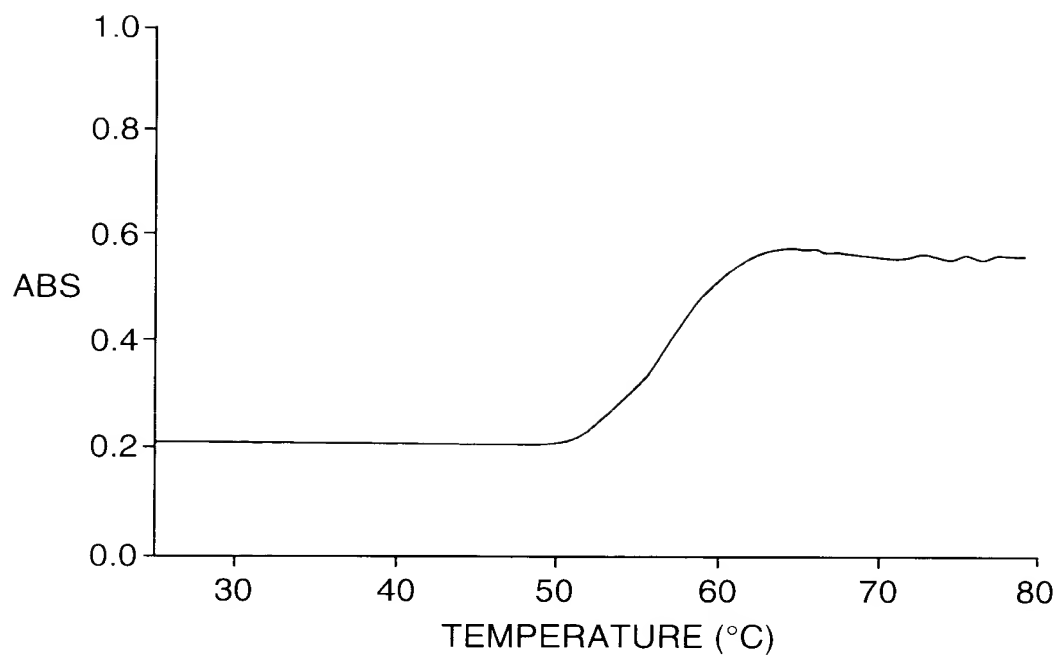


FIG. 8a

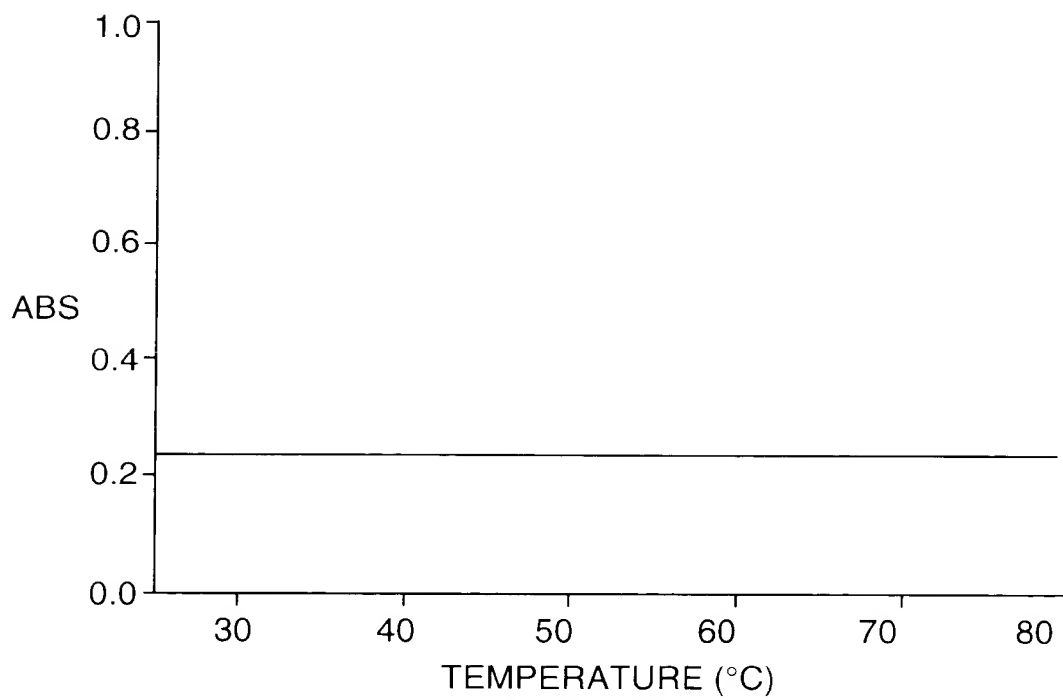


FIG. 8b

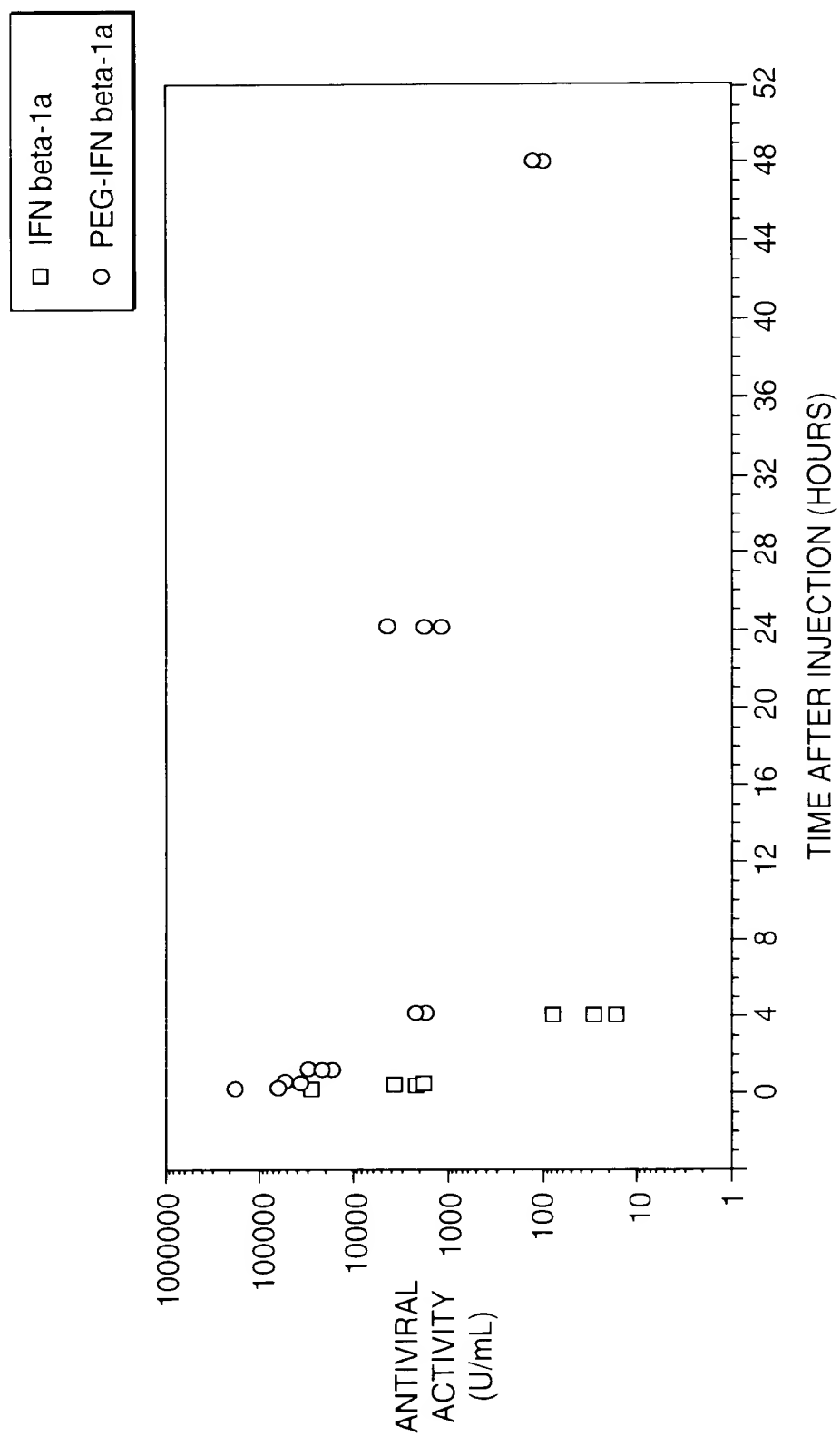


FIG. 9

1 TCCGGGGGCC ATCATCATCA TCATCATAGC TCCGGAGACG ATGATGACAA GATGAGCTAC
 AGGCCCCCGG TAGTAGTAGT AGTAGTATCG AGGCCTCTGC TACTACTGTT CTA CTCTCGATG
 1 ▶ Ser Gly Gly H i s H i s H i s H i s Ser Ser Gly Asp A s p Asp Asp L y s Met Ser Tyr
 61 AACTTGCTTG GATTCCTACA AAGAAGCAGC AATTTTCAGT GTCAGAAGCT CCTGTGGCAA
 TTGAACGAAC CTAAGGATGT TTCTTCGTCG TTA AAAAGTCA CAGTCTTCGA GGACACCGTT
 21 ▶ Asn Leu Leu G l y Phe Leu G l n Arg Ser Ser Asn Phe G l n C y s G l n L y s L e u Leu Tr p G l n
 121 TTGAATGGGA GGCTTGAATA CTGCCTCAAG GACAGGATGA ACTTTGACAT CCCTGAGGAG
 AACTTACCTT CCGA ACTTAT GACGGAGTTC CTGTCCTACT TGAAACTGTA GGGACTCCTC
 41 ▶ Leu Asn Gly A r g Leu G l u Ty r C y s Leu L y s Asp Arg Met A s n Phe Asp l l e Pr o G l u G l u
 181 ATTAAGCAGC TGCAGCAGTT CCAGAAGGAG GACGCCGCAT TGACCATCTA TGAGATGCTC
 TAATTCGTCG ACGTCGTCAA GGTCTTCCTC CTGCGGCGTA ACTGGTAGAT ACTCTACGAG
 61 ▶ l l e L y s G l n L e u G l n G l n Ph e G l n L y s G l u Asp A l a A l a L e u Thr l l e Ty r G l u Met Leu
 241 CAGAACATCT TTGCTATTTT CAGACAAGAT TCATCTAGCA CTGGCTGGAA TGAGACTATT
 GTCTTGTAGA AACGATAAAA GTCTGTTCTA AGTAGATCGT GACCGACCTT ACTCTGATAA
 81 ▶ G l n Asn l l e P h e A l a l l e Ph e Arg G l n Asp Ser Ser Ser T h r Gly Tr p As n G l u Thr l l e
 301 GTTGAGAACC TCCTGGCTAA TGTCTATCAT CAGATAAACC ATCTGAAGAC AGTCCTGGAA
 CAACTCTTGG AGGACCGATT ACAGATAGTA GTCTATTTGG TAGACTTCTG TCAGGACCTT
 101 ▶ Val G l u Asn L e u Leu A l a As n Val Tyr H i s G l n l l e Asn H i s Leu L y s Th r Val Leu G l u
 361 GAAAAACTGG AGAAAGAAGA TTTCAACCAGG GGAAAACTCA TGAGCAGTCT GCACCTGAAA
 CTTTTTGACC TCTTTCTTCT AAAGTGGTCC CTTTTTGAGT ACTCGTCAGA CGTGGACTTT
 121 ▶ G l u L y s Leu G l u L y s G l u As p Phe Thr Arg Gly L y s Leu M e t Ser Ser L e u H i s Leu L y s
 421 AGATATTATG GGAGGATTCT GCATTACCTG AAGGCCAAGG AGTACAGTCA CTGTGCCTGG
 TCTATAATAC CCTCCTAAGA CGTAATGGAC TTCCGGTTCC TCATGTCACT GACACGGACC
 141 ▶ Arg Tyr Tyr G l y Arg l l e L e u H i s Tyr Leu L y s A l a L y s G l u Tyr Ser H i s C y s A l a Tr p
 481 ACCATAGTCA GAGTGGAAAT CCTAAGGAAC TTTTACTTCA TTAACAGACT TACAGGTTAC
 TGGTATCAGT CTCACCTTTA GGATTCCTTG AAAATGAAGT AATTGTCTGA ATGTCCAATG
 161 ▶ Thr l l e Val A r g Val G l u l l e Leu Arg Asn Phe Tyr Phe l l e Asn Arg L e u Thr Gly Tyr
 541 CTCCGAAAC
 GAGGCTTTG
 181 ▶ Leu Arg Asn

FIG. 10

FIG. 11

